

SEQUENCE LISTING

<110> Syrrx, Inc.
 <120> CRYSTALLIZATION OF DIPEPTIDYL PEPTIDASE IV (DPPIV)
 <130> SYR-DPPIV-5001-C1
 <140> Not Yet Assigned
 <141> 2003-09-09
 <150> US 60/409,206
 <151> 2002-09-09
 <160> 3
 <170> PatentIn version 3.1
 <210> 1
 <211> 766
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> Amino acid sequence for full-length human wild type DPPIV
 <222> (1)..(766)
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 <308> Genbank/NP_001926
 <309> 2002-02-19
 <313> (1)..(766)
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Met Lys Thr Pro Trp Lys Val Leu Leu Gly Leu Leu Gly Ala Ala Ala
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Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
 20 25 30

Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr
 35 40 45

Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser
 50 55 60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn
 65 70 75 80

Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp
 85 90 95

Glu	Phe	Gly	His	Ser	Ile	Asn	Asp	Tyr	Ser	Ile	Ser	Pro	Asp	Gly	Gln	100	105	110	
Phe	Ile	Leu	Leu	Glu	Tyr	Asn	Tyr	Val	Lys	Gln	Trp	Arg	His	Ser	Tyr	115	120	125	
Thr	Ala	Ser	Tyr	Asp	Ile	Tyr	Asp	Leu	Asn	Lys	Arg	Gln	Leu	Ile	Thr	130	135	140	
Glu	Glu	Arg	Ile	Pro	Asn	Asn	Thr	Gln	Trp	Val	Thr	Trp	Ser	Pro	Val	145	150	155	160
Gly	His	Lys	Leu	Ala	Tyr	Val	Trp	Asn	Asn	Asp	Ile	Tyr	Val	Lys	Ile	165	170	175	
Glu	Pro	Asn	Leu	Pro	Ser	Tyr	Arg	Ile	Thr	Trp	Thr	Gly	Lys	Glu	Asp	180	185	190	
Ile	Ile	Tyr	Asn	Gly	Ile	Thr	Asp	Trp	Val	Tyr	Glu	Glu	Glu	Val	Phe	195	200	205	
Ser	Ala	Tyr	Ser	Ala	Leu	Trp	Trp	Ser	Pro	Asn	Gly	Thr	Phe	Leu	Ala	210	215	220	
Tyr	Ala	Gln	Phe	Asn	Asp	Thr	Glu	Val	Pro	Leu	Ile	Glu	Tyr	Ser	Phe	225	230	235	240
Tyr	Ser	Asp	Glu	Ser	Leu	Gln	Tyr	Pro	Lys	Thr	Val	Arg	Val	Pro	Tyr	245	250	255	
Pro	Lys	Ala	Gly	Ala	Val	Asn	Pro	Thr	Val	Lys	Phe	Phe	Val	Val	Asn	260	265	270	
Thr	Asp	Ser	Leu	Ser	Ser	Val	Thr	Asn	Ala	Thr	Ser	Ile	Gln	Ile	Thr	275	280	285	
Ala	Pro	Ala	Ser	Met	Leu	Ile	Gly	Asp	His	Tyr	Leu	Cys	Asp	Val	Thr	290	295	300	
Trp	Ala	Thr	Gln	Glu	Arg	Ile	Ser	Leu	Gln	Trp	Leu	Arg	Arg	Ile	Gln	305	310	315	320

Asn	Tyr	Ser	Val	Met	Asp	Ile	Cys	Asp	Tyr	Asp	Glu	Ser	Ser	Gly	Arg	325	330	335	
Trp	Asn	Cys	Leu	Val	Ala	Arg	Gln	His	Ile	Glu	Met	Ser	Thr	Thr	Gly	340	345	350	
Trp	Val	Gly	Arg	Phe	Arg	Pro	Ser	Glu	Pro	His	Phe	Thr	Leu	Asp	Gly	355	360	365	
Asn	Ser	Phe	Tyr	Lys	Ile	Ile	Ser	Asn	Glu	Glu	Gly	Tyr	Arg	His	Ile	370	375	380	
Cys	Tyr	Phe	Gln	Ile	Asp	Lys	Lys	Asp	Cys	Thr	Phe	Ile	Thr	Lys	Gly	385	390	395	400
Thr	Trp	Glu	Val	Ile	Gly	Ile	Glu	Ala	Leu	Thr	Ser	Asp	Tyr	Leu	Tyr	405	410	415	
Tyr	Ile	Ser	Asn	Glu	Tyr	Lys	Gly	Met	Pro	Gly	Gly	Arg	Asn	Leu	Tyr	420	425	430	
Lys	Ile	Gln	Leu	Ser	Asp	Tyr	Thr	Lys	Val	Thr	Cys	Leu	Ser	Cys	Glu	435	440	445	
Leu	Asn	Pro	Glu	Arg	Cys	Gln	Tyr	Tyr	Ser	Val	Ser	Phe	Ser	Lys	Glu	450	455	460	
Ala	Lys	Tyr	Tyr	Gln	Leu	Arg	Cys	Ser	Gly	Pro	Gly	Leu	Pro	Leu	Tyr	465	470	475	480
Thr	Leu	His	Ser	Ser	Val	Asn	Asp	Lys	Gly	Leu	Arg	Val	Leu	Glu	Asp	485	490	495	
Asn	Ser	Ala	Leu	Asp	Lys	Met	Leu	Gln	Asn	Val	Gln	Met	Pro	Ser	Lys	500	505	510	
Lys	Leu	Asp	Phe	Ile	Ile	Leu	Asn	Glu	Thr	Lys	Phe	Trp	Tyr	Gln	Met	515	520	525	
Ile	Leu	Pro	Pro	His	Phe	Asp	Lys	Ser	Lys	Lys	Tyr	Pro	Leu	Leu	Leu	530	535	540	

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg
 545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
 565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
 580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
 595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
 610 615 620

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
 625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
 645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
 660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
 675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
 690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
 705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr
 725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr
 740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro
 755 760 765

<211> 2184
<212> DNA
<213> Homo sapiens

<220>
<221> Human cDNA sequence encoding residues 39-766 of DPPIV
<222> (1)..(2184)
<223>

<400> 2
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tccttaagat ggatttcaga tcatgaatat ctctacaaac aagaaaataa tatcttggtta 120

ttcaatgctg aatatggaaa cagctcagtt ttcttggaaga acagtacatt tgatgagttt 180

ggacattcta tcaatgatta ttcaatatct cctgatgggc agtttattct cttagaatac 240

aactacgtga agcaatggag gcattcctac acagcttcat atgacattta tgatttaaata 300

aaaaggcagc tgattacaga agagaggatt ccaaacaaca cacagtgggt cacatgggtca 360

ccagtgggtc ataaattggc atatgtttgg aacaatgaca tttatgttaa aattgaacca 420

aatttaccaa gttacagaat cacatggacg gggaaagaag atataatata taatggaata 480

actgactggg tttatgaaga ggaagtcttc agtgccact ctgctctgtg gtggtctcca 540

aacggcactt ttttagcata tgcccaattt aacgacacag aagtccact tattgaatac 600

tccttctact ctgatgagtc actgcagtac ccaaagactg tacgggttcc atatccaaag 660

gcaggagctg tgaatccaac tgtaaagttc tttgttgtaa atacagactc tctcagctca 720

gtcaccaatg caacttccat acaaatcact gctcctgctt ctatgttgat aggggatcac 780

tacttggtg atgtgacatg ggcaacacaa gaaagaattt ctttgcagtg gctcaggagg 840

attcagaact attcgggtcat ggatatttgt gactatgatg aatccagtgg aagatggaac 900

tgcttagtg cagggcaaca cattgaaatg agtactactg gctgggttgg aagatttagg 960

ccttcagaac ctcatTTTtac cttgatggg aatagcttct acaagatcat cagcaatgaa 1020

gaagggttaca gacacatttg ctattttccaa atagataaaa aagactgcac atttattaca 1080

aaaggcacct gggaagtcac cgggatagaa gctctaacca gtgattatct atactacatt 1140

agtaatgaat ataaaggaat gccaggagga aggaatcttt ataaaatcca acttattgac 1200

tatacaaaag tgacatgcct cagttgtgag ctgaatccgg aaagggtgca gtactattct 1260

gtgtcattca gtaaagaggc gaagtattat cagctgagat gttccgggtc tggctctgcc 1320

ctctatactc tacacagcag cgtgaatgat aaagggtgga gagtcctgga agacaattca 1380

gctttggata aaatgctgca gaatgtccag atgccctcca aaaaactgga cttcattatt 1440

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ttcagactga actggggccac ttaccttgca agcacagaaa acattatagt agctagcttt 1620
gatggcagag gaagtgggta ccaaggagat aagatcatgc atgcaatcaa cagaagactg 1680
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gtcctgggat cggaagtgg cgtgttcaag tgtggaatag ccgtggcgcc tgtatcccg 1860
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gagtacctcc ttattcatgg aacagcagat gataacgttc actttcagca gtcagctcag 2040
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<210> 3
<211> 740
<212> PRT
<213> Homo sapiens

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<220>
<221> Amino acid sequence for residues 39-766 of DPPIV
<222> (13)..(740)
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<220>
<221> Amino acid sequence for residues 39-766 of DPPIV with N-terminal 6x-
histidine tag
<222> (1)..(740)
<223> N-terminal 6x-histidine tag (residues 1-12)

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<400> 3

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Ala Asp Pro Gly Gly Ser His His His His His His Ser Arg Lys Thr
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Tyr Thr Leu Thr Asp Tyr Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr
          20          25          30

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Ser Leu Arg Trp Ile Ser Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn
          35          40          45

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Asn Ile Leu Val Phe Asn Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu
50 55 60

Glu Asn Ser Thr Phe Asp Glu Phe Gly His Ser Ile Asn Asp Tyr Ser
65 70 75 80

Ile Ser Pro Asp Gly Gln Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys
85 90 95

Gln Trp Arg His Ser Tyr Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn
100 105 110

Lys Arg Gln Leu Ile Thr Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp
115 120 125

Val Thr Trp Ser Pro Val Gly His Lys Leu Ala Tyr Val Trp Asn Asn
130 135 140

Asp Ile Tyr Val Lys Ile Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr
145 150 155 160

Trp Thr Gly Lys Glu Asp Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val
165 170 175

Tyr Glu Glu Glu Val Phe Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro
180 185 190

Asn Gly Thr Phe Leu Ala Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro
195 200 205

Leu Ile Glu Tyr Ser Phe Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys
210 215 220

Thr Val Arg Val Pro Tyr Pro Lys Ala Gly Ala Val Asn Pro Thr Val
225 230 235 240

Lys Phe Phe Val Val Asn Thr Asp Ser Leu Ser Ser Val Thr Asn Ala
245 250 255

Thr Ser Ile Gln Ile Thr Ala Pro Ala Ser Met Leu Ile Gly Asp His
260 265 270

Tyr Leu Cys Asp Val Thr Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln
275 280 285

Trp Leu Arg Arg Ile Gln Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr
290 295 300

Asp Glu Ser Ser Gly Arg Trp Asn Cys Leu Val Ala Arg Gln His Ile
305 310 315 320

Glu Met Ser Thr Thr Gly Trp Val Gly Arg Phe Arg Pro Ser Glu Pro
325 330 335

His Phe Thr Leu Asp Gly Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu
340 345 350

Glu Gly Tyr Arg His Ile Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys
355 360 365

Thr Phe Ile Thr Lys Gly Thr Trp Glu Val Ile Gly Ile Glu Ala Leu
370 375 380

Thr Ser Asp Tyr Leu Tyr Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro
385 390 395 400

Gly Gly Arg Asn Leu Tyr Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val
405 410 415

Thr Cys Leu Ser Cys Glu Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser
420 425 430

Val Ser Phe Ser Lys Glu Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly
435 440 445

Pro Gly Leu Pro Leu Tyr Thr Leu His Ser Ser Val Asn Asp Lys Gly
450 455 460

Leu Arg Val Leu Glu Asp Asn Ser Ala Leu Asp Lys Met Leu Gln Asn
465 470 475 480

Val Gln Met Pro Ser Lys Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr
485 490 495

Lys Phe Trp Tyr Gln Met Ile Leu Pro Pro His Phe Asp Lys Ser Lys
 500 505 510

Lys Tyr Pro Leu Leu Leu Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys
 515 520 525

Ala Asp Thr Val Phe Arg Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr
 530 535 540

Glu Asn Ile Ile Val Ala Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln
 545 550 555 560

Gly Asp Lys Ile Met His Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu
 565 570 575

Val Glu Asp Gln Ile Glu Ala Ala Arg Gln Phe Ser Lys Met Gly Phe
 580 585 590

Val Asp Asn Lys Arg Ile Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr
 595 600 605

Val Thr Ser Met Val Leu Gly Ser Gly Ser Gly Val Phe Lys Cys Gly
 610 615 620

Ile Ala Val Ala Pro Val Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr
 625 630 635 640

Thr Glu Arg Tyr Met Gly Leu Pro Thr Pro Glu Asp Asn Leu Asp His
 645 650 655

Tyr Arg Asn Ser Thr Val Met Ser Arg Ala Glu Asn Phe Lys Gln Val
 660 665 670

Glu Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn Val His Phe Gln
 675 680 685

Gln Ser Ala Gln Ile Ser Lys Ala Leu Val Asp Val Gly Val Asp Phe
 690 695 700

Gln Ala Met Trp Tyr Thr Asp Glu Asp His Gly Ile Ala Ser Ser Thr
 705 710 715 720

Ala His Gln His Ile Tyr Thr His Met Ser His Phe Ile Lys Gln Cys

725

730

735

Phe Ser Leu Pro
740